SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> A gene encoding an enzyme catalyzing biosynthesis of lignan, and the use thereof

<130> SU0411/PCT

<150> JP 2003-341313
<151> 2003-09-30

<150> JP 2003-432383
<151> 2003-12-26

<160> 79

<170> PatentIn Ver. 2.1

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Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser
        355                 360                 365

Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly
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Gly Tyr Asn Val Pro Lys Gly Thr Met Val Leu Val Asn Ala Trp Ala
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Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro
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            420                 425                 430

Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe
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<210> 4
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<210> 5

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<212> DNA
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<220>
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<210> 6
<211> 18
<212> DNA
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<220>
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<210> 7
<211> 24
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<210> 8
<211> 18
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<210> 9
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<210> 10
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<210> 13
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<210> 15
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<210> 16
<211> 18
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<210> 17
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<210> 18
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<210> 19
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<210> 20
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<210> 21
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<210> 22
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<400> 22
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<210> 23
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<210> 24
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<210> 25
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<210> 26
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<210> 28
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<400> 28
agaaacctct ctggttta 18

<210> 29
<211> 24
<212> DNA
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<210> 30
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<210> 31
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<210> 32
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<400> 32
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<210> 33
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<210> 34
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<212> DNA
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<210> 35
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<210> 36
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<212> DNA
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<210> 37
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<210> 38
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<400> 42
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Arg Pro Pro Gly Pro Pro Gly Leu Pro Phe Leu Gly Asn Leu Leu Gln
35 40 45

Tyr Asn Pro Ser Asp Leu His Leu Arg Leu Thr Lys Leu Ser Glu Lys
50 55 60

Tyr Gly Pro Leu Met Tyr Met Thr Phe Val Gly Lys Pro Val Val Val
65 70 75 80

Ile Ser Ser Ala Arg Val Ala Lys Glu Ala Leu Lys Tyr Asn Asp Leu
85 90 95

Ala Phe Ser Ser Arg Pro Ser Thr Ile Ala Ser Arg Lys Val Ala Tyr
100 105 110

Asn Asn Ser Asp Ile Ser Met Ser Pro Tyr Thr Glu Tyr Trp Arg Glu
115 120 125

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Leu Arg Lys Met Val Val Leu Arg Leu Phe Thr Val Lys Gln Val Asn
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Ser Phe Arg Pro Ala Arg Glu Glu Glu Val Ala Arg Met Val Lys Glu
145                 150                 155                 160

Ile Ser Arg Arg Ala Asn Ala His Gln Pro Val Asn Ile Asn Glu Ile
                165                 170                 175

Ala Leu Ser Leu Ser Ser Arg Met Ile Ser Arg Phe Ala Leu Gly Lys
            180                 185                 190

Arg Tyr Asp Glu Glu Asn Gly Pro Glu Lys Arg Arg Phe Asp Arg Ile
        195                 200                 205

Leu Gln Leu Leu Gln Leu Val Ser Val Glu Ile Phe Phe Gly Asp Tyr
    210                 215                 220

Ser Pro Trp Leu Gly Trp Ile Asp Arg Leu Cys Gly Lys Val Ser Gln
225                 230                 235                 240

Leu Glu Lys Ala Phe Lys Asp Leu Asp Ser Leu Tyr Glu Glu Met Ile
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Ala Glu His Leu Ser Pro Asn Arg Pro Glu Ser Met Asn Gly Asp Ile
            260                 265                 270

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln
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Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala
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Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu
305                 310                 315                 320

Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser
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            340                 345                 350

Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro
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Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp
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Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala
385                 390                 395                 400

Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro
                405                 410                 415

Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly
            420                 425                 430

Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu
        435                 440                 445

Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe
    450                 455                 460
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His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp
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gatcctgaga atgttcacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300
aagttcaggg aaatttttga tgttcttgga gatgggattt tcaatgcaga ttcggagtcc 360
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ctggcgaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tgaaacggtg 480
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acttgtacat ttgttactgg ttatgatcct ggatgcttgt ctgttgattt gcctgatgtt 600
cctttctcga aagccctaga tgatgccgaa gaagcgatat tcatgcgcca tgtggttcct 660
gaaaagattt ggaaacttca gaggtggttt ggggttggat ctgagagaaa attgagcaag 720
gctcgtgaag tcttggatag cgtcattggc aggtatatcg cgctgaagcg cggcgaaatg 780
agaagccgag gaatttcgat tgattgtgaa aatgaagatg gtgtggatct gctcacgtct 840
tacatgactg tgggagacga tggtactcaa acccatgatt tgaaatgtga tgacaagttc 900
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cacgagccct catacaagtt cttggctttc aatgctggtc cgaggacttg cttggggaag 1380
gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt 1440
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<210> 56
<211> 515
<212> PRT
<213> Sesamum indicum

<220>
<223> SiP288

<400> 56
Met Val Gly Ile Val Tyr Ile Glu Leu Phe Leu Ser Val Met Trp Phe
1 5 10 15

Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp
20 25 30

Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile

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         35                  40                  45

His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe
     50                  55                  60

His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala
 65                  70                  75                  80

Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe
                 85                  90                  95

Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly
            100                 105                 110

Ile Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala
        115                 120                 125

Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile
    130                 135                 140

Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val
145                 150                 155                 160

Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu
                165                 170                 175

Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys
            180                 185                 190

Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp
        195                 200                 205

Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp
    210                 215                 220

Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys
225                 230                 235                 240

Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys
                245                 250                 255

Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu
            260                 265                 270

Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly
        275                 280                 285

Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr
    290                 295                 300

Ile Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu
305                 310                 315                 320

Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg
                325                 330                 335

Ile Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys
            340                 345                 350

Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His
        355                 360                 365

Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln
```

370 375 380

His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val
385 390 395 400

Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met
405 410 415

Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp
420 425 430

Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu
435 440 445

Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe
450 455 460

Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val
465 470 475 480

His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu
485 490 495

Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala
500 505 510

Lys Lys Asn
515

<210> 57
<211> 1494
<212> DNA
<213> Sesamum indicum

<220>
<223> SiP168

<400> 57
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aaacctcttc ccataatcgg caacattctt gagcttggtg agaaacccca ccaatctctc 180
gccaaactct ccaaaaccta cgggcccctg atgcgtctca agctgggaac catgacaaca 240
gttgttgtat cctccccgga aatctccagg atcgtgctgc aacaatatga ccaagttttc 300
tccagccgaa cacacgcaga tgccatccga gcacttgacc accacaaaca ttccgtcgcc 360
tggataccgg cggacaatca gtggcggaaa atccgtaaac tgtgcaaaga gaagatgttt 420
tcgggccaaa agcttgatgc gaaccagggc ctgaggaggg agaagttgcg taatttgcaa 480
gactatgtga atgaatgctg cgttagtggc caggtcgtgg atattggtgt agctgccttt 540
acgacgaccc ttaatctgat atcggccact cttttctcgg tggattttgc tgattttggt 600
tctggttcgt ctcaagagct taaggatgtt atgagcggga tagcgtctat catcggccga 660
ccaaattttg ctgattgttt ccctcttctt cggctggttg atccacaggg catcttccgc 720
cagaccacgt tacatttcaa caagtgtttt aagatctttg atgaaattat ccgtcaaagg 780
ctacagacca atgattcggg gacgaaaagt gacatgctga aagagcttct tgaaatcaac 840
cagaaagatg agtctgaatt gagctttgac gagatcaagc atttactcct ggatctactt 900
gtcgcaggaa cggacacaac ttcagttaca gtggaatggg caatgacgga gctagtgcgc 960
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ttcaggcttc accctgcaac tcctttatcg gtacctcaca aggccgacga ggaagcagaa 1140
atcaatggct atatagtccc taaaggagca caagttctca tgaacgtgtg ggccatcggc 1200
agagattcaa gcatatggag gaaccctgat gtattcatgc ccgagaggtt cttggagaca 1260
gaaattgatg tccgtggcca acacttcgag ctgcttcctt ttggcggggg gaggaggatt 1320
tgcgtggggc tgccgttagc ctatcgtatg atccatctcg tgcttgccac tttcataagc 1380
gactatgatt ggaaacttga aggagggctg aaaactgaag aaatggacat gagtgaaaag 1440

ttcggcctca ccctgcaaaa agccattcct ctcaaggcac ttccagttaa aatt 1494

<210> 58
<211> 498
<212> PRT
<213> Sesamum indicum

<220>
<223> SiP168

<400> 58
Met Asp Leu Leu Leu Ser Leu Val Leu Leu Leu Cys Ser Ala Ala Cys
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Ile Trp Phe Leu Arg Val Val Leu Lys Pro Asn Pro Gly Pro Arg Lys
20 25 30

Ser Ala Asn Leu Pro Pro Gly Pro Lys Pro Leu Pro Ile Ile Gly Asn
35 40 45

Ile Leu Glu Leu Gly Glu Lys Pro His Gln Ser Leu Ala Lys Leu Ser
50 55 60

Lys Thr Tyr Gly Pro Leu Met Arg Leu Lys Leu Gly Thr Met Thr Thr
65 70 75 80

Val Val Val Ser Ser Pro Glu Ile Ser Arg Ile Val Leu Gln Gln Tyr
85 90 95

Asp Gln Val Phe Ser Ser Arg Thr His Ala Asp Ala Ile Arg Ala Leu
100 105 110

Asp His His Lys His Ser Val Ala Trp Ile Pro Ala Asp Asn Gln Trp
115 120 125

Arg Lys Ile Arg Lys Leu Cys Lys Glu Lys Met Phe Ser Gly Gln Lys
130 135 140

Leu Asp Ala Asn Gln Gly Leu Arg Arg Glu Lys Leu Arg Asn Leu Gln
145 150 155 160

Asp Tyr Val Asn Glu Cys Cys Val Ser Gly Gln Val Val Asp Ile Gly
165 170 175

Val Ala Ala Phe Thr Thr Thr Leu Asn Leu Ile Ser Ala Thr Leu Phe
180 185 190

Ser Val Asp Phe Ala Asp Phe Gly Ser Gly Ser Ser Gln Glu Leu Lys
195 200 205

Asp Val Met Ser Gly Ile Ala Ser Ile Ile Gly Arg Pro Asn Phe Ala
210 215 220

Asp Cys Phe Pro Leu Leu Arg Leu Val Asp Pro Gln Gly Ile Phe Arg
225 230 235 240

Gln Thr Thr Leu His Phe Asn Lys Cys Phe Lys Ile Phe Asp Glu Ile
245 250 255

Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met
260 265 270

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Leu Lys Glu Leu Leu Glu Ile Asn Gln Lys Asp Glu Ser Glu Leu Ser
        275                 280                 285

Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr
    290                 295                 300

Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg
305                 310                 315                 320

His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val
                325                 330                 335

Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr
            340                 345                 350

Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro
        355                 360                 365

Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr
    370                 375                 380

Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly
385                 390                 395                 400

Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg
                405                 410                 415

Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu
            420                 425                 430

Pro Phe Gly Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr
        435                 440                 445

Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp
    450                 455                 460

Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys
465                 470                 475                 480

Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val
                485                 490                 495

Lys Ile
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<210> 59
<211> 1545
<212> DNA
<213> Sesamum indicum

<220>
<223> SiP236

<400> 59
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aggtaccatc ccattggtgg taccgtgttc aaccagctgc tgaacttcta taggttgcat 180
gattatatgg ctgatcttgc agggaagtac aagacttaca gactgattgc ccctttcgg 240
actgaggtct atacatctga ccccgctaat gttgagcaca tgttgaaaac gaatttcgaa 300
agttatggca agggacctta caattgcagc attctggggg atttgtttgg tgaaggaatt 360
ttcgcaatcg atggccataa gtggagggag cagagaaaag tgtcaagcct tgagttttct 420
acaagggttc tgagggatta cagtagcatc gtcttcagga aaaacgccgt aaggctcgca 480

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aaaattctgt ctggagctgc aacttccaac caaccagtgg atattcaaga tcttttcatg 540
aaatcaactt ttgattctat ttcggaagtt gctttaggag ttgagcttga cagcttgggt 600
ggttcaaatg aagaaggtgc caaatttagc attgctgcag acgacgtgag tatgaggaca 660
ctttggagat acgtggatgt tctgtggaag ttaaagagag ctctaaatgt tggttcagaa 720
gcaaaactga agaaaagcct tcaagtggtt gatgaatttg tgtataagct gattcatagt 780
aggactcagc aaatgaacat gccaggaaat gattctgtta tgcagctgaa gaaagacgac 840
attttgtcaa gattcttgca acttactgag gccactccca agtacttgag ggacataaca 900
ataagcttta tagttgctgg taaagacaca acagcaacaa ctctctcctg gtttatttac 960
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gcggtggatg caaagcaatg tttgtgtgat gatataatgc cggatgggtt cagtgttaag 1200
aaggggaca tggtggctta tcaaccatat gcaatgggaa ggatgaaatc catatggggt 1260
aatgatgcag aagagttcaa accagagaga tggcttgaca aaaacggttg cttccagcag 1320
gccagccctt ttaagtttac agctttccag gccggccctc gtctttgttt ggggaaagag 1380
tttgcttatc ggcagatgaa gatattctca gccattctgc tgagattctt taccatgaaa 1440
ctaagtgatg aaagaaagac agtaaactac agaccaatgc tcactcttct catcgacggt 1500
ggtctcattg tccgcccctt tcacagaatg gacgagaaaa ctgca                 1545
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<210> 60
<211> 515
<212> PRT
<213> Sesamum indicum

<220>
<223> SiP236

<400> 60

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Met Ala Asn Pro Ile Asp Phe Leu Leu Ser Pro Thr Pro Tyr Val Ala
  1               5                  10                  15

Thr Thr Leu Leu Tyr Val Leu Phe Ser Val Leu Ile Val Arg Phe Leu
             20                  25                  30

Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr
         35                  40                  45

Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala
     50                  55                  60

Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg
 65                  70                  75                  80

Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys
                 85                  90                  95

Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu
            100                 105                 110

Gly Asp Leu Phe Gly Glu Gly Ile Phe Ala Ile Asp Gly His Lys Trp
        115                 120                 125

Arg Glu Gln Arg Lys Val Ser Ser Leu Glu Phe Ser Thr Arg Val Leu
    130                 135                 140

Arg Asp Tyr Ser Ser Ile Val Phe Arg Lys Asn Ala Val Arg Leu Ala
145                 150                 155                 160

Lys Ile Leu Ser Gly Ala Ala Thr Ser Asn Gln Pro Val Asp Ile Gln
                165                 170                 175

Asp Leu Phe Met Lys Ser Thr Phe Asp Ser Ile Ser Glu Val Ala Leu
```

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            180                 185                 190

Gly Val Glu Leu Asp Ser Leu Gly Gly Ser Asn Glu Glu Gly Ala Lys
        195                 200                 205

Phe Ser Ile Ala Ala Asp Asp Val Ser Met Arg Thr Leu Trp Arg Tyr
    210                 215                 220

Val Asp Val Leu Trp Lys Leu Lys Arg Ala Leu Asn Val Gly Ser Glu
225                 230                 235                 240

Ala Lys Leu Lys Lys Ser Leu Gln Val Val Asp Glu Phe Val Tyr Lys
                245                 250                 255

Leu Ile His Ser Arg Thr Gln Gln Met Asn Met Pro Gly Asn Asp Ser
            260                 265                 270

Val Met Gln Leu Lys Lys Asp Asp Ile Leu Ser Arg Phe Leu Gln Leu
        275                 280                 285

Thr Glu Ala Thr Pro Lys Tyr Leu Arg Asp Ile Thr Ile Ser Phe Ile
    290                 295                 300

Val Ala Gly Lys Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Ile Tyr
305                 310                 315                 320

Met Leu Cys Lys Tyr Pro His Val Gln Glu Lys Val Glu Gln Glu Ile
                325                 330                 335

Lys Asp Ala Thr Gly Cys Lys Glu Val Ala Asp Ile Ser Glu Phe Ser
            340                 345                 350

Ala Cys Val Thr Glu Glu Ala Leu Gly Lys Met His Tyr Leu His Ala
        355                 360                 365

Ala Leu Thr Glu Thr Leu Arg Ile Tyr Pro Ala Val Ala Val Asp Ala
    370                 375                 380

Lys Gln Cys Leu Cys Asp Asp Ile Met Pro Asp Gly Phe Ser Val Lys
385                 390                 395                 400

Lys Gly Asp Met Val Ala Tyr Gln Pro Tyr Ala Met Gly Arg Met Lys
                405                 410                 415

Ser Ile Trp Gly Asn Asp Ala Glu Glu Phe Lys Pro Glu Arg Trp Leu
            420                 425                 430

Asp Lys Asn Gly Cys Phe Gln Gln Ala Ser Pro Phe Lys Phe Thr Ala
        435                 440                 445

Phe Gln Ala Gly Pro Arg Leu Cys Leu Gly Lys Glu Phe Ala Tyr Arg
    450                 455                 460

Gln Met Lys Ile Phe Ser Ala Ile Leu Leu Arg Phe Phe Thr Met Lys
465                 470                 475                 480

Leu Ser Asp Glu Arg Lys Thr Val Asn Tyr Arg Pro Met Leu Thr Leu
                485                 490                 495

Leu Ile Asp Gly Gly Leu Ile Val Arg Pro Phe His Arg Met Asp Glu
            500                 505                 510

Lys Thr Ala
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515

<210> 61
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, Bam-SST-FW2

<400> 61
tggatcccaa ctcatagagt actcaaaaac gctt 34

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-Nco-RV

<400> 62
gcaaatgatc aaccatggtg ttct 24

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SST-RV1

<400> 63
cacatgaacg agacgaactg ggtttgg 27

<210> 64
<211> 506
<212> PRT
<213> Sesamum radiatum

<220>
<223> SrSiP189

<400> 64
Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile
1 5 10 15

Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Gln Glu Lys Ser Ser Leu
20 25 30

Ile Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His
35 40 45

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Val His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser
     50                  55                  60

Gln Lys Leu Gly Pro Ile Phe Ser Leu Arg Phe Gly Thr Arg Leu Val
 65                  70                  75                  80

Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr
                 85                  90                  95

Asp Ile Val Leu Ala Asn Arg Pro Gln Pro Ser Val Asp Arg Arg Ser
            100                 105                 110

Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His
        115                 120                 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr
    130                 135                 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met
145                 150                 155                 160

Ile Ser Ser Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn
                165                 170                 175

Leu Glu Thr Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met
            180                 185                 190

Val Ala Gly Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu
        195                 200                 205

Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser
    210                 215                 220

Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Phe
225                 230                 235                 240

Asn Gly Leu Glu Lys Lys Leu Ala Val His Ala Arg Lys Thr Asp Glu
                245                 250                 255

Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn
            260                 265                 270

Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr
        275                 280                 285

Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala
    290                 295                 300

Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Ile
305                 310                 315                 320

Leu Asn His Pro Gln Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr
                325                 330                 335

Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu
            340                 345                 350

Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser
        355                 360                 365

Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly
    370                 375                 380
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Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Leu Val Asn Ala Trp Ala
385                 390                 395                 400

Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro
                405                 410                 415

Asp Arg Phe Glu Thr Met Glu Val Glu Thr His Lys Leu Leu Pro Phe
            420                 425                 430

Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe
        435                 440                 445

Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Glu Trp Glu Arg
    450                 455                 460

Met Ser Ala Glu Lys Ile Asp Leu Asn Glu Gly Ser Gly Ile Thr Leu
465                 470                 475                 480

Pro Lys Ala Lys Thr Leu Glu Ala Met Cys Lys Pro Arg His Ile Met
                485                 490                 495

Glu Arg Val Leu Arg Gln Val Ser Asn Val
            500                 505
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<210> 65
<211> 1518
<212> DNA
<213> Sesamum radiatum

<220>
<223> SrSiP189

<400> 65

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ggttggctcc cggtgatcgg ccacgttcat ctcatgaaaa atctcctcca tagaacacta 180
tacgacttct cccagaaact gggacccata ttttccctcc ggttcggcac ccgcctcgtg 240
gtagtggtgt cctcctcctc cctggtcgag gaatgtttca ccaagtacga cattgtcttg 300
gccaaccgcc ctcagccctc tgtcgaccgg cgctcactcg ggttcagcac caccagcgta 360
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atttcgtcgt tgtacaaaat ctcgtccgcc ggtttcgcga aggtgaattt ggagacgaag 540
attgttgagc tgacgtttaa taacataatg aggatggtgg cggggaagag atactatggg 600
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gagttgacga gcgcttccaa tcctggtgag atatttccaa tattgcggtg gcttggtttc 720
aatgggttgg agaagaagct ggctgttcac gcgcggaaga cggatgagtt catgcaaggg 780
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ttgcaggaat ctcaacctga gtactacact gatgaaatca tcactggcct catagttgca 900
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gagaccttaa ggttatttcc ttctgttcca acgttggtgc cacacgaacc atcggaggat 1140
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atacaccgag accccaaggt gtgggacgac cccttgagct ttaagcccga caggtttgag 1260
acaatggaag tggagacaca caagctgttg ccgttcggga tgggcaggag agcgtgtccc 1320
ggagctggat tggcgcagaa gtttgtgggg ttggctttgg ggtcgctgat tcagtgtttc 1380
gagtgggaga gaatgagtgc ggagaaaatt gacttgaacg aaggttctgg gataaccttg 1440
cctaaagcta agacgttgga agccatgtgc aaacctagac atatcatgga gagagttctt 1500
cgtcaggttt cgaacgtc                                              1518
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<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, NtUBQ-FW

<400> 66
ggaatgcaga tcttcgtcaa 20

<210> 67
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, NtUBQ-RW

<400> 67
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<210> 68
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, SiP189-bam-FW

<400> 68
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<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, SiP189-nco-RV

<400> 69
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<210> 70
<211> 25
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<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, STAR-LF1

<400> 70

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<210> 71
<211> 25
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<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, STAR-LR1

<400> 71
ccacctgacg tcgcggccta atacg 25

<210> 72
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, M13-47(F)

<400> 72
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<210> 73
<211> 24
<212> DNA
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<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, RV-M(R)

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<210> 74
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<212> DNA
<213> Sesamun indium

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<210> 75
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, gSST-FW1

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<210> 76
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence, gSST-RV2

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ctgcgaatta gaaagaattc tgtaaaccat 30

<210> 77
<211> 2815
<212> DNA
<213> Sesamum radiatum

<220>
<221> misc_feature
<222> (2199)..(2199)
<223> n stands for any base

<400> 77
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<211> 507
<212> PRT
<213> Sesumum alatum

<400> 78

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Leu His Leu Ile Lys Asn Pro Leu His Arg Thr Leu Tyr Asp Cys Ser
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Gln Lys Leu Gly Ser Ile Phe Ser Val Trp Phe Gly Ser Arg Leu Val
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Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr
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Asp Ile Val Leu Ala Asn Arg Pro Asp Leu His Leu Asp Leu Arg Ser
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Arg Leu Ala Ser Phe Leu Ser Ile Arg Arg Asp Glu Arg Asp Arg Met
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Leu Ala Gly Lys Ile Tyr Tyr Gly Glu Glu Ala Glu Asp Glu Glu Glu
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Ala Lys Arg Phe Arg Asp Met Thr Lys Glu Ala Leu Glu Leu Met Asn
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Asn Gly Phe Glu Lys Gln Leu Pro Val His Ser Arg Lys Thr Asp Glu
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Ile Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn
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Thr Met Val Gly His Leu Leu Ser Leu Gln Glu Ser Gln Pro Asp Tyr
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355 360 365

Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Asn Ile Gly
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Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Ile Val Asn Ala Trp Ala
385 390 395 400

Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Met Ser Phe Lys Pro
405 410 415

Asp Arg Phe Glu Thr Leu Glu Val Glu Thr His Lys Leu Leu Pro Phe
420 425 430

Gly Met Gly Arg Arg Gly Cys Pro Gly Ala Gly Leu Ala Lys Lys Phe
435 440 445

Val Gly Leu Ala Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Glu Arg
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<212> DNA
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